

Figure S1. Apoptosis and cell cycle analyses in acute myeloid leukemia lines under pulsed kevetrin treatment. Representative histograms of Annexin V staining in (A) MOLM-13 and (B) KASUMI-1 cells treated with different concentrations of kevetrin (85, 170 and 340  $\mu$ M) for 6 and 6+66 h wo (x3). Representative histograms of PI staining for cell cycle analysis in (C) MOLM-13 and (D) KASUMI-1 cells untreated or treated with kevetrin 340  $\mu$ M for 6 and 6+66 h wo (x3). KEV, kevetrin; wo, washout; CTRL, control; PI, propidium iodide.

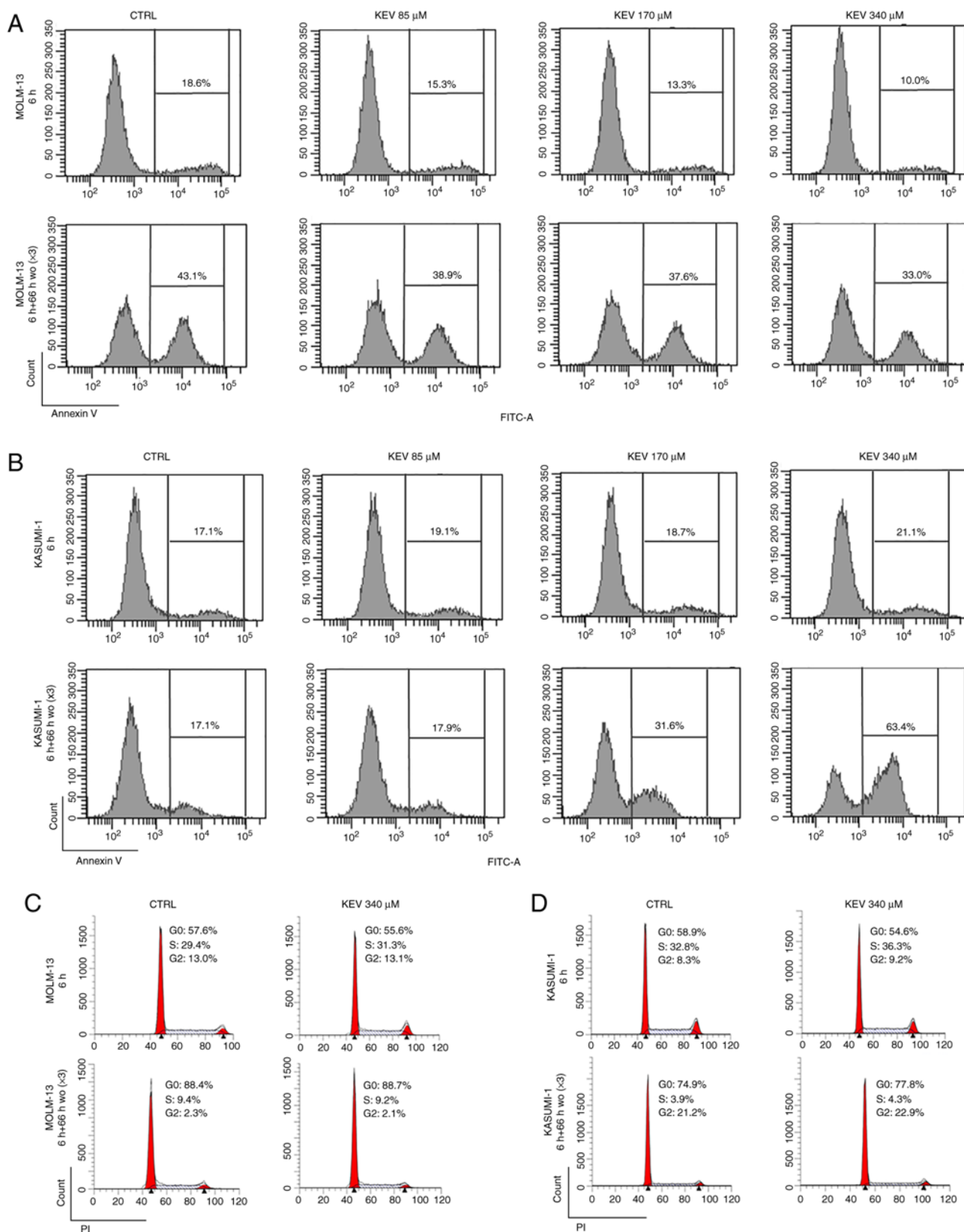


Figure S2. Viability of acute myeloid leukemia cell lines after 72 h of kevetrin treatment. Viability of OCI-AML3, MOLM-13, KASUMI-1 and NOMO-1 cell lines treated with different concentrations of kevetrin (85, 170 and 340  $\mu\text{M}$ ) for 72 h. Values represent the mean  $\pm$  standard deviation of three biological replicates. \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

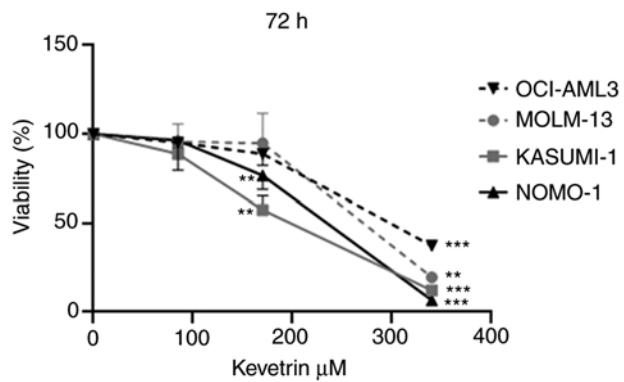


Figure S3. Apoptosis analysis in acute myeloid leukemia cell lines under 24 h of continuous kevetrin treatment. Representative histograms of Annexin V staining in OCI-AML3, MOLM-13, KASUMI-1 and NOMO-1 cells treated with different concentrations of kevetrin (85, 170 and 340  $\mu$ M) for 24 h. KEV, kevetrin; CTRL, control.

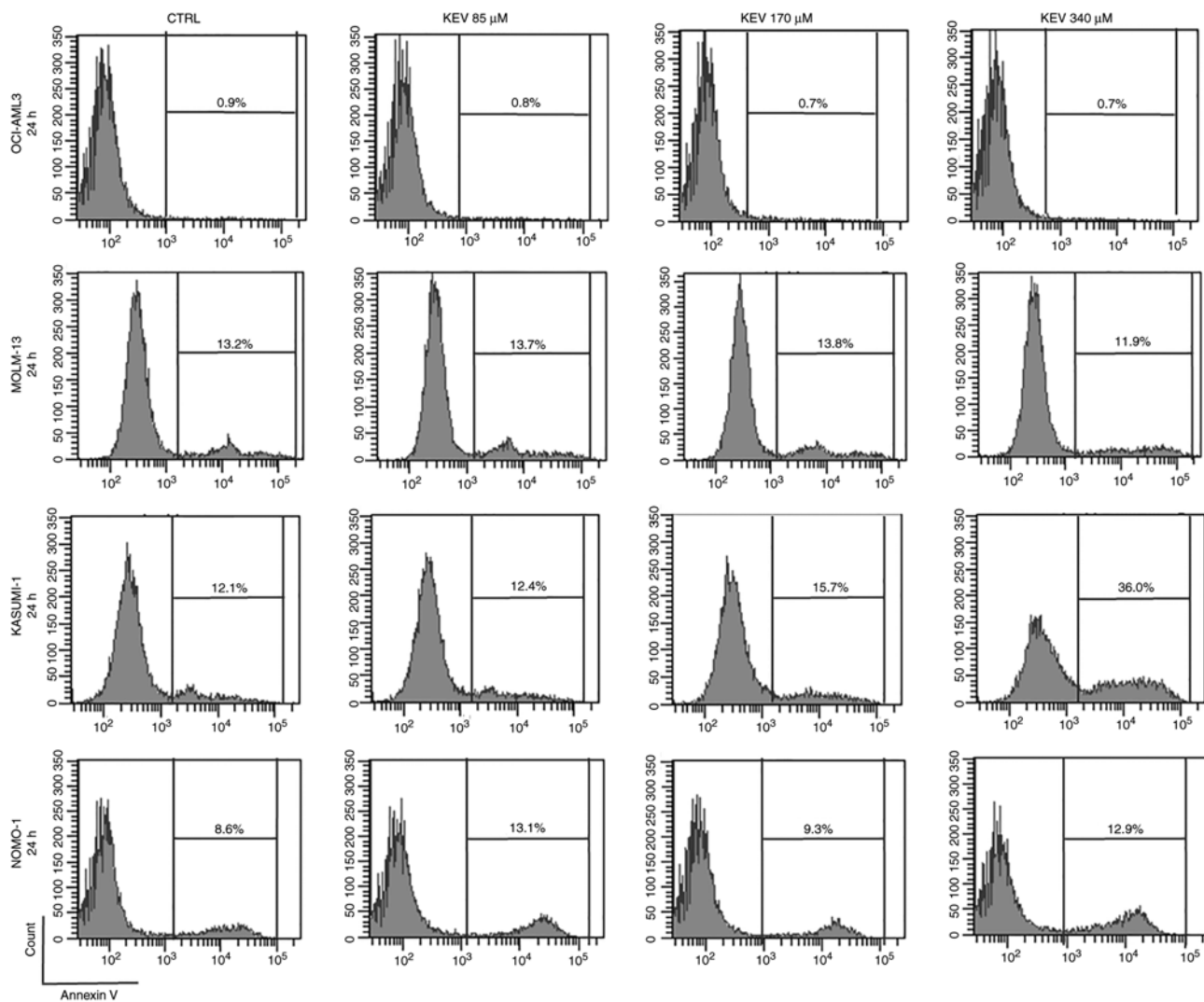


Figure S4. Apoptosis analysis in acute myeloid leukemia cell lines under 48 h of continuous kevetrin treatment. Representative histograms of Annexin V staining in OCI-AML3, MOLM-13, KASUMI-1 and NOMO-1 cells treated with different concentrations of kevetrin (85, 170 and 340  $\mu$ M) for 48 h. KEV, kevetrin; CTRL, control.

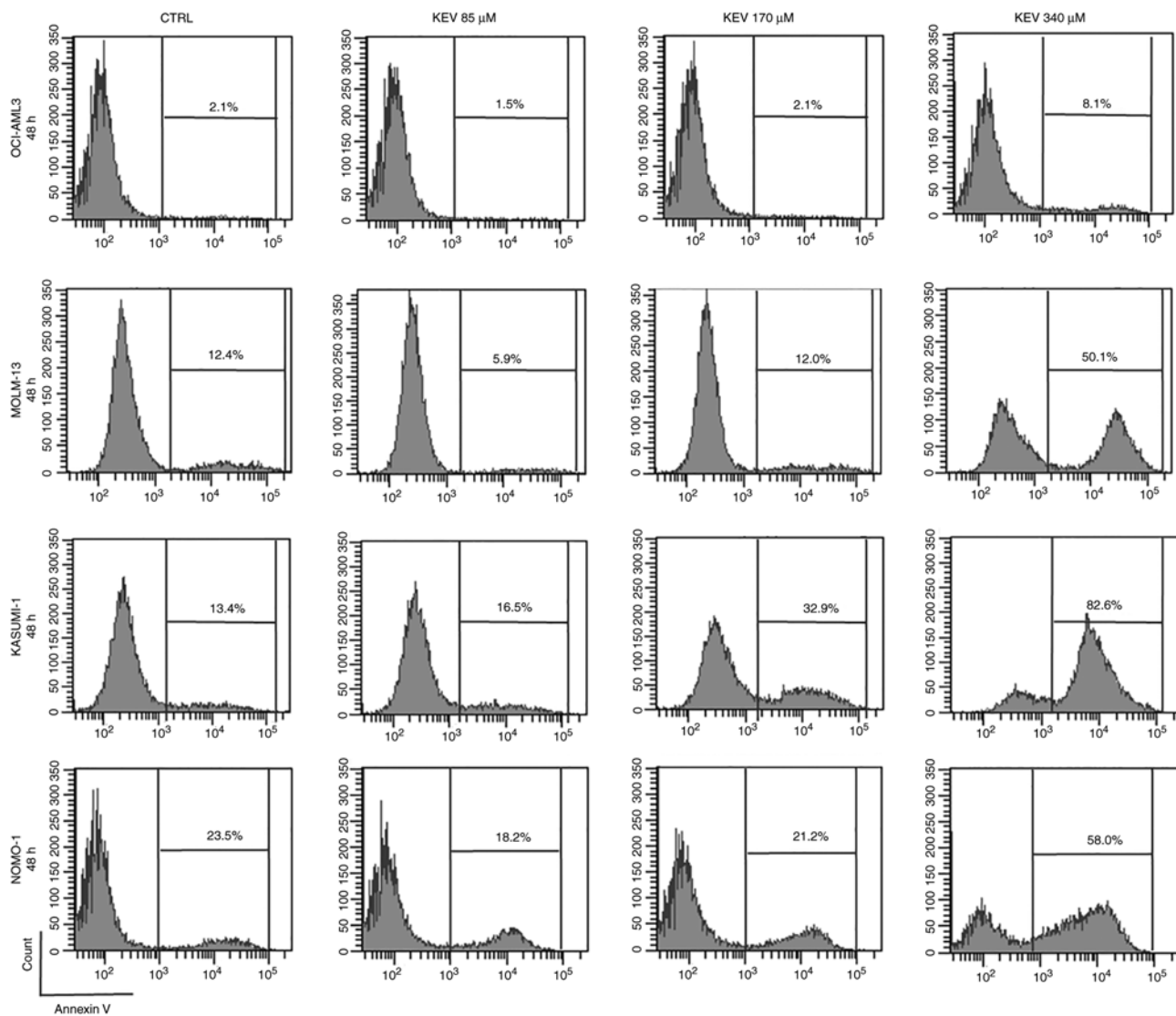


Figure S5. Apoptosis analyses in acute myeloid leukemia cell lines under continuous kevetrin treatment. Quantification of mitochondrial depolarization in (A) MOLM-13 and (B) KASUMI-1 treated with kevetrin (85, 170 and 340  $\mu$ M) for 24 and 48 h. (C) Percentage of TUNEL<sup>+</sup> MOLM-13 and (D) KASUMI-1 cells after 24 and 48 h treatment with kevetrin 340  $\mu$ M. Percentage of (E) MOLM-13 and (F) KASUMI-1 cells with active caspase-3 after 24 and 48 h of treatment with kevetrin 340  $\mu$ M. Values represent the mean  $\pm$  standard deviation of three biological replicates (\* $P$ <0.05, \*\* $P$ <0.01, \*\*\* $P$ <0.001). KEV, kevetrin; CTRL, control.

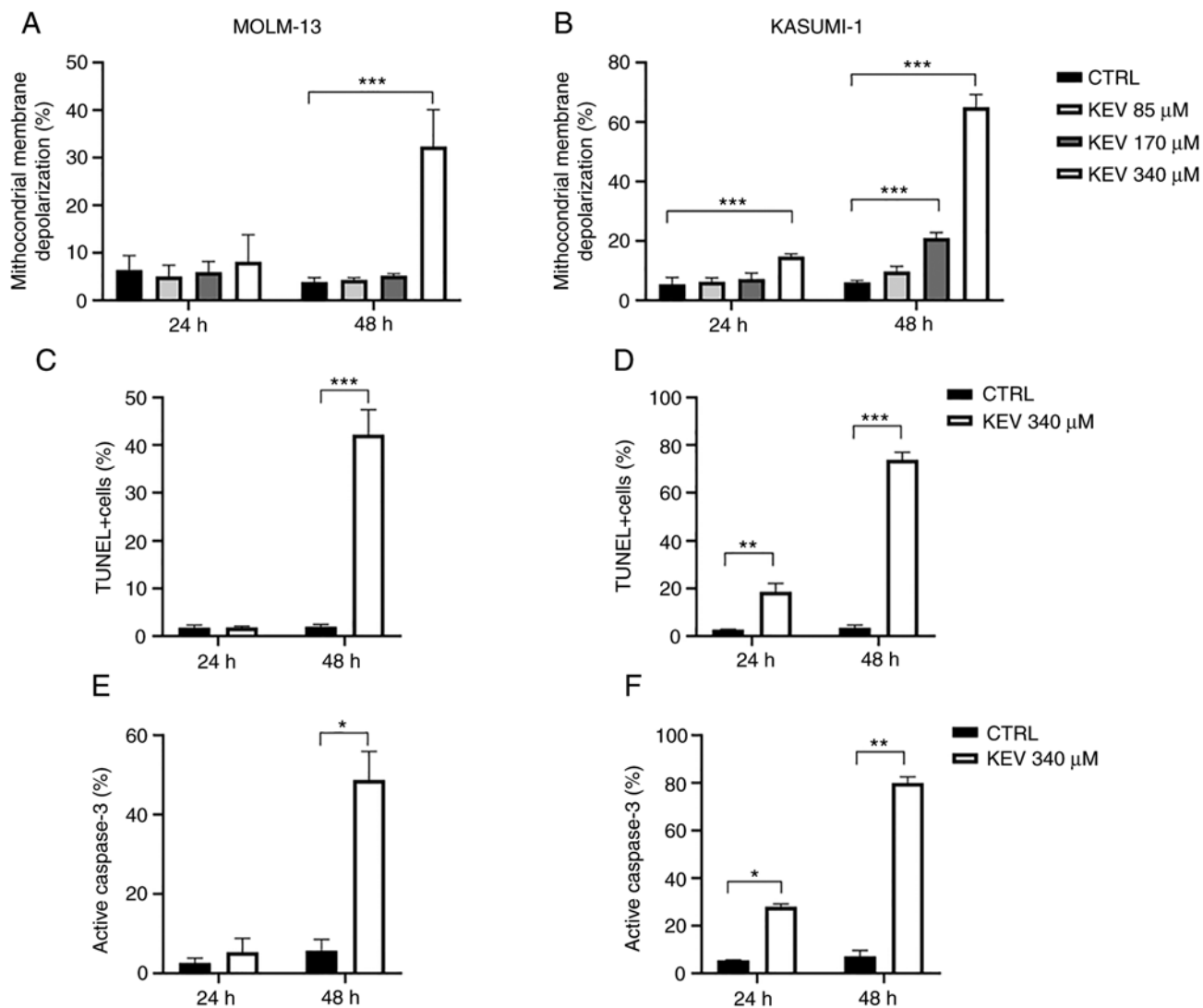


Figure S6. Cell cycle analysis in AML cell lines and apoptosis analysis in primary AML cells under continuous kevetrin treatment. Representative histograms of PI staining for cell cycle analysis in (A) OCI-AML3, (B) MOLM-13, (C) KASUMI-1 and (D) NOMO-1 cells untreated and treated with kevetrin 340  $\mu$ M for 24 and 48 h. (E) Representative histograms of Annexin V staining in primary AML bone marrow mononuclear cells after 48 h of treatment with increasing concentrations of kevetrin (85, 170 and 340  $\mu$ M). AML, acute myeloid leukemia; KEV, kevetrin; CTRL, control; PI, propidium iodide.

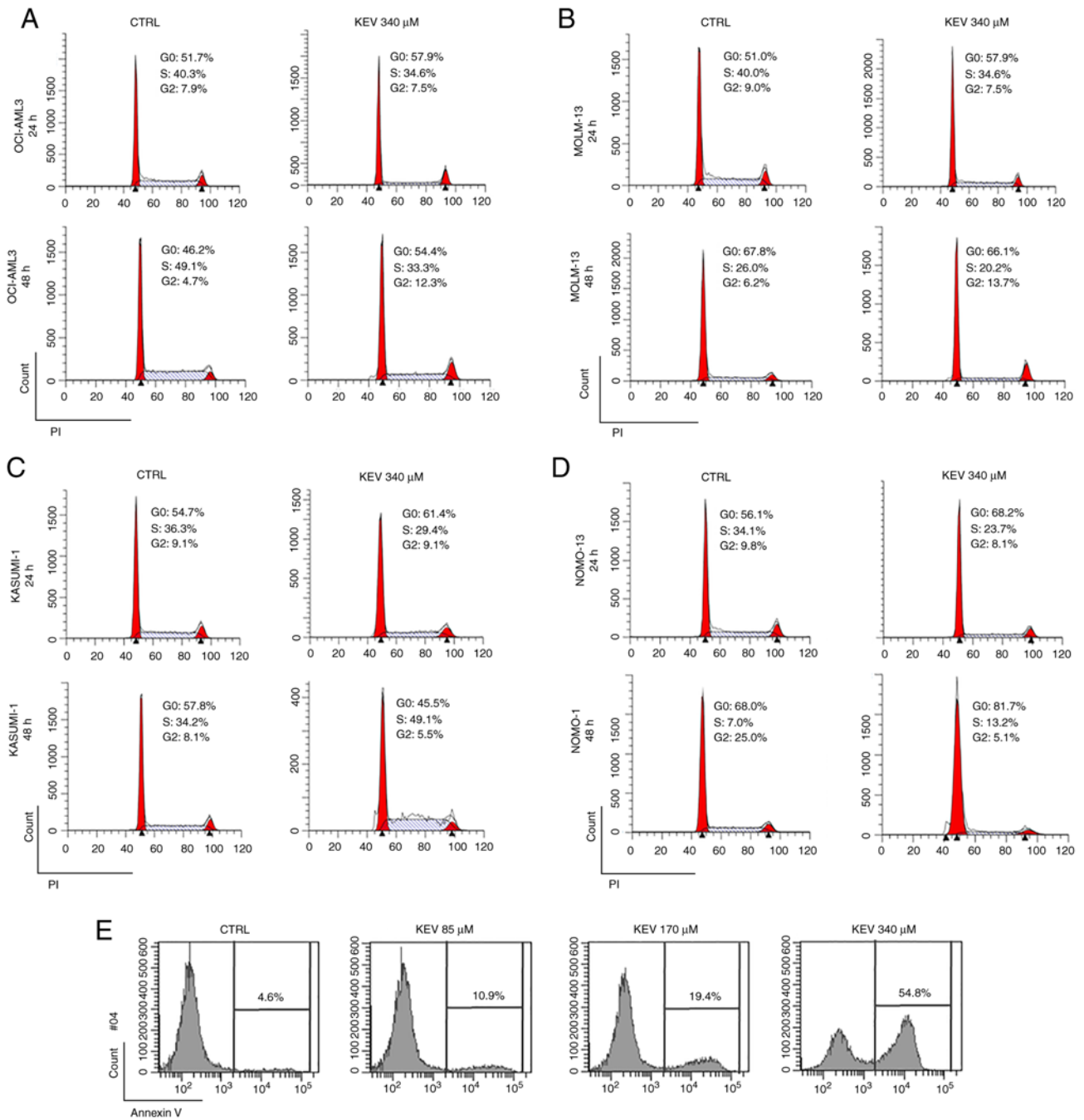


Table SI. Characteristics of primary AML cases.

Patient no.	Sex	Age, years	Karyotype
1	F	81	44,XX,-3,del(5)(q13q31),-6-7,add(11)(q22),+mar[8]/46,XX,-3,del(5)(q13q31),-6,-7,add(11)(q22),+3mar[3]/46,XX,del(5)(q13q31)[1]
2	M	85	46,XY[5]
3	M	72	46,XY[20]
4	M	83	Not available

AML, acute myeloid leukemia; F, female; M, male.

Table SII. Targeted next-generation sequencing of primary acute myeloid leukemia samples.

Patient no.	Gene	Locus	NM_ID	Exon	Type	Coding	Amino acid change	VAF (%)	Coding consequence	Depth
1	<i>DNMT3A</i>	Chr2:25467099	NM_022552	15	SNP	c.1776C>A	p.(Tyr592*)	44	Nonsense	10531
1	<i>JAK2</i>	Chr9:5072576	NM_004972	13	SNP	c.1726A>G	p.(Thr576Ala)	48.1	Missense	10144
1	<i>TP53</i>	Chr17:7577517	NM_000546	7	SNP	c.764T>A	p.(Ile255Asn)	92.3	Missense	9526
2	<i>ASXL1</i>	Chr20:31021211	NM_015338	12	SNP	c.1210C>T	p.(Arg404*)	47	Nonsense	7756
2	<i>CEBPA</i>	Chr19:33792731	NM_004364	1	INDEL	c.584_589dup	p.(His195_Pro196dup)	48.6	Inframe_6	3779
2	<i>U2AF1</i>	Chr21:44514777	NM_006758	6	SNP	c.470A>G	p.(Gln157Arg)	7	Missense	7780
2	<i>TET2</i>	Chr4:106158147	NM_017628	3	SNP	c.3048T>G	p.(Cys1016Trp)	48.8	Missense	8584
2	<i>TET2</i>	Chr4:106156187	NM_017628	3	SNP	c.1088C>T	p.(Pro363Leu)	49.3	Missense	7848
3	<i>DNMT3A</i>	Chr2:25457242	NM_022552	23	SNP	c.2645G>A	p.(Arg882His)	44.7	Missense	6168
3	<i>FLT3</i>	Chr13:28608263	NM_004119	14	INDEL	c.1792_1793ins27	p.(Tyr597_Glu598ins9)	46.1	Inframe_27	6049
3	<i>NPM1</i>	Chr5:1.71E+08	NM_002520	11	INDEL	c.863_864insCCTG	p.(Trp288Cysfs*?)	45.4	Frameshift	6176
3	<i>CSF3R</i>	Chr1:36935408	NM_000760	11	SNP	c.1319G>A	p.(Arg440Gln)	48.6	Missense	5400
4	<i>CEBPA</i>	Chr19:33793028	NM_004364	1	INDEL	c.292dupA	p.(Thr98Asnfs*10)	47.4	Frameshift	2764
4	<i>CEBPA</i>	Chr19:33792990	NM_004364	1	SNP	c.331G>T	p.(Ala111Ser)	58.7	Missense	2068
4	<i>FLT3</i>	Chr1328608086	NM_004119	15	INDEL	c.1718_1879dup	p.(Asn626_Ala627ins84)	70.1	Inframe_252	7652
4	<i>FLT3</i>	Chr1328592634	NM_004119	20	INDEL	c.2508_2510del	p.(Ile836del)	13.4	Inframe_3	7857
4	<i>NPM1</i>	Chr5:170837543	NM_002520	11	INDEL	c.860_863dup	p.(Trp288Cysfs*?)	42.8	Frameshift	7281
4	<i>TET2</i>	Chr4:106155604	NM_017628	3	INDEL	c.507_508del	p.(His169Glnfs*6)	47.6	Frameshift	8167
4	<i>TET2</i>	Chr4:106180835	NM_001127208	7	SNP	c.3863G>T	p.(Gly1288Val)	43.5	Missense	6470



Table SIII. Pathway enrichment of upregulated genes.

	ID	Term	Gene symbols	P-value
<b>Transcription</b>				
1	GO:0006351	Transcription DNA-templated	CREBFR, ZNF559, EZH1, CTNND1, ZNF10, LPXN, ZNF227, ZNF776, ZNF226, CIR1, TSPYL2, HEXIM1, BCAS3, ZNF266, PLAG1, NFKBIZ, SAP18, HES1, NCOA1, NCOA3, ID2, ID1	0.0037
2	GO:0006355	Regulation of transcription DNA-templated	CREBFR, ZNF559, CTNND1, ZNF10, ELL2, HES1, LPXN, NCOA1, ZNF227, ZNF776, ZNF226, TSPYL2, NCOA3, CDKN2AIP, PARP14, ZNF484, ZNF266, TP53INP1, GOLGB1	0.0257
3	GO:0006352	DNA-templated transcription, initiation	HIST4H4, HIST2H4B, HIST1H4H	0.0285
<b>Signaling pathways</b>				
4	hsa04668	TNF signaling pathway	CASP10, PTGS2, JUN, RIPK1, CASP8, MAP3K8, NFKBIA, IL1B	4.96 E-05
5	GO:0051092	Positive regulation of NF- $\kappa$ B transcription factor activity	TRIM38, RIPK1, NFKBIA, IL1B, HSPA1A, HSPA1B	0.0030
6	GO:0043123	Positive regulation of I- $\kappa$ B kinase/NF- $\kappa$ B signaling	S100A4, CASP10, TRIM38, PLK2, RIPK1, CASP8, TLR6	0.0012
7	hsa04064	NF- $\kappa$ B signaling pathway	PTGS2, RIPK1, NFKBIA, IL1B	0.0464
8	hsa04620	Toll-like receptor signaling pathway	JUN, RIPK1, CASP8, MAP3K8, TLR1, NFKBIA, IL1B, TLR6	4.96 E-05
9	GO:0045410	Positive regulation of inter leukin-6 biosynthetic process	TLR1, IL1B, TLR6	0.0014
10	GO:0032757	Positive regulation of inter leukin-8 production	RIPK1, IL1B, HSPA1A, HSPA1B	0.0009
11	hsa04010	MAPK signaling pathway	DUSP1, JUN, MAP3K8, DUSP10, IL1B, HSPA1A, HSPA1B, GADD45B	0.0089
12	GO:0000188	Inactivation of MAPK activity	DUSP1, DUSP10, DUSP22	0.0143
<b>Cell death</b>				
13	hsa04210	Apoptosis	CASP10, RIPK1, CASP8, NFKBIA	0.0194
14	GO:2001240	Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	RIPK1, IL1B, HSPA1A, HSPA1B	0.0025
15	GO:0010941	Regulation of cell death	JUN, HSPA1A, HSPA1B	0.0028
<b>Telomeres</b>				
16	GO:0032200	Telomere organization	HIST4H4, HIST1H3H, HIST2H4B, HIST1H4H	0.0010
17	GO:0016233	Telomere capping	HIST4H4, HIST2H4B, HIST1H4H	0.0122
<b>Nucleosome assembly</b>				
18	GO:0006334	Nucleosome assembly	HIST4H4, TSPYL2, HIST2H2BE, HIST1H3H, HIST2H4B, HIST1H4H	0.0018
19	GO:0006335	DNA replication-dependent nucleosome assembly	HIST4H4, HIST1H3H, HIST2H4B, HIST1H4H	0.0016
20	GO:0006336	DNA replication-independent nucleosome assembly	HIST4H4, HIST2H4B, HIST1H4H	0.0154
21	GO:0034080	CENP-A containing nucleosome assembly	HIST4H4, HIST2H4B, HIST1H4H	0.0395

Table SIII. Continued.

	ID	Term	Gene symbols	P-value
Autophagy				
22	GO:0000045	Autophagosome assembly	GABARAPL1, ATG14, WIPI1, TP53INP1	0.0033
23	GO:0016236	Macroautophagy	GABARAPL1, SQSTM1, ATG14, WIPI1	0.0183
24	GO:0000422	Mitophagy	GABARAPL1, SQSTM1, WIPI1	0.0271

GO, Gene Ontology; has, *Homo sapiens*.

Table SIV. Pathway enrichment of downregulated genes.

ID	Term	Gene symbols	P-value	
Cell cycle				
1	GO:0000082	G1/S transition of mitotic cell cycle	CDC7, BCAT1, CDC6, POLA1, SKP2, MCM2, CDK4, MCM3, MCM4, CDC25A, PPAT, MCM6, PRIM1, TYMS, CDC45, MCM7, GSPT1, RRM2, FBXO5, ORC6, ORC1	1.24 E-08
2	hsa04110	Cell cycle	E2F4, E2F5, PRKDC, CDC45, MCM7, ORC6, ORC1, MYC, TFDPI1, ANAPC1, CDC7, CDC6, TP53, SKP2, MCM2, CDK4, MCM3, YWHAE, MCM4, CDC25A, MCM6, MAD2L1, HDAC2, CCND2, SMC1A	1.94 E-07
3	GO:0007077	Mitotic nuclear envelope disassembly	CTDNEP1, AAAS, SEH1L, NUP88, NUP205, NUP210, NUP155	0.0113
4	GO:0006260	DNA replication	TIPIN, POLA1, KIAA0101, NFIX, DTD1, CDC45, MCM7, ORC6, ORC1, FEN1, EXO1, CDC7, SSRP1, CDC6, POLI, RBBP4, DTL, MCM2, MCM3, MCM4, CDC25A, MCM6, RFC5, TIMELESS, RRM2, POLD1, RRM1, POLD2, SUPT16H, CHAF1B, DUT	4.04 E-12
5	hsa03030	DNA replication	RFC5, PRIM1, MCM7, POLD1, POLD2, POLA1, MCM2, MCM3, RNASEH2B, MCM4, FEN1, MCM6	4.37 E-06
6	GO:0006270	DNA replication initiation	CDC7, PRIM1, CDC6, CDC45, MCM7, POLA1, ORC6, MCM2, MCM3, MCM4, ORC1, MCM6	5.28 E-08
7	GO:0006268	DNA unwinding involved in DNA replication	MCM7, MCM2, HMGA1, MCM4, MCM6	0.0006
8	GO:0006271	DNA strand elongation involved in DNA replication	PRIM1, POLD1, POLD2, POLA1	0.0250
9	GO:0051301	Cell division	HAUS4, ASUN, TIPIN, KNTC1, CCNG1, TUBB, NCAPH, CDCA7, SEH1L, FBXO5, SKA2, USP16, TUBA1B, HELLS, CDC7, ANAPC1, CDC6, KIF18B, CDK4, PPP1CC, SMC2, NCAPD3, CDC25A, SEPT11, MAD2L1, TIMELESS, RCC2, CCND2, CENPV, CDCA7L, RUVBL1, SMC1A	0.0001
10	GO:0007067	Mitotic nuclear division	HAUS4, ANAPC1, CDC6, ASUN, NUP88, TIPIN, KNTC1, PBK, CCNG1, CDC25A, TIMELESS, RCC2, NOLC1, CENPV, FBXO5, SKA2, RUVBL1, USP16, HELLS, PPP5C	0.0118
11	GO:0051436	Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	ANAPC1, PSMB5, MAD2L1, PSMC4, PSME1, PSMD10, PSMB3, FBXO5	0.0338
12	GO:0051437	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	ANAPC1, PSMB5, MAD2L1, PSMC4, PSME1, PSMD10, PSMB3, FBXO5	0.0463
Biosynthetic processes				
13	hsa01200	Carbon metabolism	ALDOA, ME2, TALDO1, PGAM1, HK2, ESD, ACAT2, ACAT1, GOT2, PGAM4, IDH2, RPIA, ENO1, FH, SHMT2, SUCLG2, CS, PFKP, DLAT, GPI, RPE, PGK1, PSAT1, PCCB, MDH2, PRPS2, PRPS1	1.27 E-09
14	hsa01230	Biosynthesis of amino acids	BCAT1, ALDOA, SHMT2, TALDO1, ALDH18A1, CS, PFKP, PGAM1, GOT2, RPE, PGAM4, MTR, IDH2, RPIA, PGK1, PSAT1, PRPS2, ENO1, PRPS1	1.91 E-07
15	GO:0006541	Glutamine metabolic process	NIT2, CTPS1, CAD, ASNS, GMPS, PFAS	0.0014
16	GO:0006164	Purine nucleotide biosynthetic process	MTHFD1, ATIC, ADSL, HPRT1, PFAS, IMPDH2, PPAT, PRPS1	1.83 E-07

Table SIV. Continued.

	ID	Term	Gene symbols	P-value
<b>Biosynthetic processes</b>				
17	GO:0009168	Purine ribonucleoside monophosphate biosynthetic process	ATIC, ADSL, GMPS, PAICS, PFAS, IMPDH2, PPAT	8.59 E-06
18	GO:0006189	'De novo' IMP biosynthetic process	ATIC, ADSL, PAICS, PFAS, PPAT	4.90 E-05
19	GO:0009113	Purine nucleobase biosynthetic process	GMPS, PAICS, PPAT	0.0172
20	GO:0006695	Cholesterol biosynthetic process	MSMO1, SQLE, HMGCR, CYP51A1, DHCR7, INSIG1, HMGCS1, ACLY, FDFT1, DHCR24	2.71 E-05
21	hsa00100	Steroid biosynthesis	MSMO1, SQLE, CYP51A1, DHCR7, FDFT1, DHCR24	0.0053
22	GO:0008299	Isoprenoid biosynthetic process	HMGCR, HMGCS1, PDSS1, FDFT1	0.0207
23	GO:0006730	One-carbon metabolic process	MTHFD1, MTHFD2, SHMT2, AHCY, AHCYL1, ALDH1L2, MTHFD1L	0.0016
24	GO:0046655	Folic acid metabolic process	MTHFD1, MTHFD2, SHMT2, ALDH1L2, MTHFD1L	0.0066
25	GO:0046653	Tetrahydrofolate metabolic process	MTHFD2, TYMS, SHMT2, MTHFD1L	0.0077
26	GO:0035999	Tetrahydrofolate interconversion	MTHFD1, TYMS, SHMT2, MTHFD1L	0.0077
27	GO:0009396	Folic acid-containing compound biosynthetic process	MTHFD1, MTHFD2, MTHFD1L	0.0251
28	GO:0043101	Purine-containing compound salvage	ADK, MTAP, HPRT1, PNP, APRT	0.0025
29	GO:0006166	Purine ribonucleoside salvage	ADK, MTAP, HPRT1	0.0106
30	GO:0006488	Dolichol-linked oligosaccharide biosynthetic process	ALG3, SRD5A3, DPAGT1, ALG8	0.0250
31	hsa01212	Fatty acid metabolism	CPT2, SCD, MCAT, HSD17B12, ACACA, FASN, ACAT2, HADH, TECR, ACAT1	0.0018
32	GO:0006633	Fatty acid biosynthetic process	MSMO1, XBP1, MCAT, HSD17B12, ACACA, FASN, NDUFAB1, ACLY, PCCB	0.0017
33	GO:0035338	Long-chain fatty-acyl-CoA biosynthetic process	SCD, HSD17B12, ACACA, FASN, ACLY, TECR	0.0342
<b>Bioenergetics</b>				
34	GO:0006094	Gluconeogenesis	ALDOA, GOT2, GPI, SLC25A13, SLC25A10, PGAM4, PGM1, PGAM1, PGK1, G6PC3, MDH2, ENO1	1.95 E-06
35	GO:0006096	Glycolytic process	ALDOA, GPI, LDHA, PGAM4, PGM1, PGAM1, HK2, PGK1, ENO1	8.00 E-05
36	GO:0061621	Canonical glycolysis	ALDOA, GPI, PFKFB4, PGAM1, HK2, PFKP, PGK1, ENO1	8.93 E-05
37	hsa00010	Glycolysis, gluconeogenesis	ALDOA, GPI, LDHB, LDHA, PGAM4, PGM1, PGAM1, HK2, PFKP, DLAT, PGK1, G6PC3, ENO1	0.0005
38	GO:0006099	Tricarboxylic acid cycle	NNT, SUCLG2, CS, IDH2, DLAT, MDH2, FH	0.0013
39	hsa00020	Citrate cycle (TCA cycle)	SUCLG2, CS, IDH2, ACLY, DLAT, MDH2, FH	0.0074
40	hsa00620	Pyruvate metabolism	LDHB, LDHA, ME2, ACACA, GLO1, DLAT, ACAT2, ACAT1, MDH2, FH	0.0004
41	GO:0006090	Pyruvate metabolic process	LDHB, LDHA, BSG, ME2, GLO1, DLAT	0.0021
42	GO:0010827	Regulation of glucose transport	AAAS, SEH1L, NUP88, NUP205, NUP210, NUP155	0.0131
43	hsa00030	Pentose phosphate pathway	ALDOA, GPI, RPE, TALDO1, PGM1, PFKP, RPIA, PRPS2, PRPS1	0.0002
44	GO:0009052	Pentose-phosphate shunt, non-oxidative branch	RPE, TALDO1, RPIA	0.0251

Table SIV. Continued.

ID	Term	Gene symbols	P-value	
<b>Bioenergetics</b>				
45	GO:0042776	Mitochondrial ATP synthesis coupled proton transport	ATP5D, ATP5B, CYC1, STOML2, ATP5A1, ATP5G1, ATP5H	0.0002
46	GO:0006754	ATP biosynthetic process	ALDOA, ATP5D, SLC25A13, ATP5B, ATP5A1, ATP5G1, ATP5H	0.0013
47	GO:0015986	ATP synthesis coupled proton transport	ATP5D, ATP5B, ATP5A1, ATP5G1, ATP5H	0.0137
48	hsa00190	Oxidative phosphorylation	ATP5D, COX11, UQCRC1, ATP5B, NDUFA7, COX8A, CYC1, NDUFAB1, ATP5G1, COX5A, PPA1, COX6A1, ATP5A1, ATP5H, COX15	0.0256
49	GO:0006123	Mitochondrial electron, transport cytochrome <i>c</i> to oxygen	CYCS, COX8A, COX6A1, COX5A, COX15	0.0097
<b>DNA repair</b>				
50	GO:0006281	DNA repair	XRCC2, UNG, POLA1, BCCIP, INTS3, NONO, CHD1L, FANCI, ACTL6A, APEX1, ERCC1, FEN1, EXO1, SSRP1, POLI, TRIM28, GTF2H3, RAD54L, RFC5, DOT1L, UHRF1, POLD1, PARPBP, SUPT16H, UCHL5, RUVBL1, SMC1A, CHAF1B, ALKBH2, UBE2T, PPP5C	1.16 E-07
51	GO:0006283	Transcription-coupled nucleotide-excision repair	RFC5, PRPF19, POLR2E, POLD1, POLD2, POLR2I, GTF2H3, ERCC1	0.0410
52	GO:0006296	Nucleotide-excision repair, DNA incision, 5'-to lesion	RFC5, CHD1L, POLD1, POLD2, GTF2H3, ERCC1	0.0209
53	GO:0033683	Nucleotide-excision repair, DNA incision	RFC5, CHD1L, POLD1, POLD2, GTF2H3, ERCC1	0.0232
54	GO:0070911	Global genome nucleotide-excision repair	UBE2N, SUMO2, CHD1L, GTF2H3, ERCC1	0.0482
55	hsa03430	Mismatch repair	EXO1, RFC5, POLD1, POLD2, MLH1, MLH3	0.0099
56	GO:0006298	Mismatch repair	EXO1, POLD1, MSH5, POLD2, MLH1, MLH3	0.0167
<b>Translation</b>				
57	GO:0006406	mRNA export from nucleus	AAAS, SEH1L, NUP88, NUP205, NUP210, ALYREF, THOC6, EIF5A, NUP155	0.0686
58	GO:0006412	Translation	MRPL42, MRPS15, PABPC4, MRPL11, RPL34, SLC25A23, MRPL37, GUF1, RMND1, RPSA, MRPL3, DARS, SLC25A5, SLC25A6, GTF2H3, MRPS21, MRRF, MRPL24, MRPL21, SLC25A13, SLC25A10, FARSB, SLC25A19, RPS13, SLC25A39	0.0003
59	GO:0006418	tRNA aminoacylation for protein translation	YARS, NARS, DARS, GARS, EPRS, WARS2, DARS2, IARS2, VARS, KARS, PPA1, IARS, FARSB, LARS	6.99 E-09
60	GO:0006450	Regulation of translational fidelity	IARS, LARS, YRDC, IARS2, VARS, DTD1	0.0003
61	hsa00970	Aminoacyl-tRNA biosynthesis	YARS, NARS, DARS, GARS, EPRS, WARS2, DARS2, IARS2, VARS, KARS, IARS, FARSB, LARS	0.0004
62	GO:0001731	Formation of translation preinitiation complex	EIF3C, EIF3D, EIF3CL, EIF3B, EIF3E, EIF3F, EIF3K, EIF2S3, EIF3I, EIF3M	2.43 E-07
63	GO:0006446	Regulation of translational initiation	EIF3C, EIF3D, EIF3CL, EIF3B, EIF3E, EIF3F, DDX1, EIF3K, EIF3I, EIF2B2, EIF3M	2.01 E-06
64	GO:0006413	Translational initiation	EIF6, ABCE1, RPSA, EIF2S3, EIF2A, LARP1, EIF3C, EIF3CL, EIF3D, EIF3B, EIF1AX, EIF3E, RPL34, EIF3F, EIF3K, RPS13, EIF3I, EIF2B2, EIF3M	2.64 E-05

Table SIV. Continued.

ID	Term	Gene symbols	P-value	
Translation				
65	GO:0000460	Maturation of 5.8S rRNA	EIF6, MAK16, RRP15, LAS1L	0.0168
66	GO:0000470	Maturation of LSU-rRNA	EIF6, MAK16, RRP15, LAS1L	0.0250
67	GO:1904851	Positive regulation of establishment of protein localization to telomere	CCT7, CCT5, CCT4, DKC1, CCT8, CCT2	1.65 E-05
68	GO:0006409	tRNA export from nucleus	XPOT, AAAS, SEH1L, NUP88, NUP205, NUP210, NUP155	0.0022
Telomeres				
69	GO:0032212	Positive regulation of telomere maintenance via telomerase	CCT7, CCT5, CCT4, DKC1, CCT8, CCT2	0.0115
70	GO:0000722	Telomere maintenance via recombination	RFC5, PRIM1, POLD1, POLD2, POLA1, FEN1	0.0115
Splicing				
71	GO:0000387	Spliceosomal snRNP assembly	CLNS1A, PRMT5, SNRPD3, SNRPB, SNRPD1, SNRPF, GEMIN4, GEMIN5	0.0001
72	GO:0000398	mRNA splicing, via spliceosome	FUS, SNRPA1, POLR2E, PPIL1, SNRPD3, ALYREF, PTBP1, POLR2I, SNRPD1, HNRNPR, HNRNPU, PRPF19, NONO, HNRNPA3, HNRNPL, NUDT21, DHX15, SNRPB, SNRPA, SNRPF, GEMIN5	0.0016
GO, Gene Ontology; has, <i>Homo sapiens</i> .				